This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-24 (canceled)

Claim 25. (allowed) A method of assessing an individual's predisposition to a selected calcification condition status, namely a lower peak bone mass, which method comprises determining the genotype of the promoter of the bone sialoprotein gene (SEQ ID NO 25) to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the bone sialoprotein gene, wherein said allelic variation is selected from (a) said promoter including the sequence

ATATAGAAGCCCAAG-**G**-AAAATCAGCTGACC (SEQ ID NO 18)
including guanine at the marked position rather than the sequence
ATATAGAAGCCCAAG-**A**-AAAATCAGCTGACC (SEQ ID NO 13)
including adenine at the marked position, said sequence occurring in said promoter at a position spanning approximately base pair 1496 of the sequence of said gene having the sequence set forth as SEQ ID NO 25
and (b) said promoter including the sequence
ATAGTGAAAACTTGT-**A**-TAATTATGAAATTTT (SEQ ID NO 19)
including adenine at the marked position rather than the sequence
ATAGTGAAAACTTGT-**G**-TAATTATGAAATTTT (SEQ ID NO 14)
including guanine at the marked position, said sequence occurring in said promoter at a position spanning approximately base pair 1869 of the sequence of said gene having the sequence set forth as SEQ ID NO 25,
and associating the presence of said adenine in said sequence spanning base pair 1496 bp with a predisposition to a lower peak bone mass than when guanine is present and the

presence of said guanine in said sequence spanning base pair 1869 bp with a predisposition to a lower peak bone mass than when adenine is present.

Claim 26. (previously amended) A method as claimed in Claim 25, which further comprises determining the genotype of the promoter of the matrix gla protein gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the matrix gla protein gene, wherein said allelic variation is said promoter including the sequence

TGGCTGGCTGGCTGG-**A**-TGGATGGATG (SEQ ID NO 20)

including adenine at the marked position rather than the sequence

TGGCTGGCTGGCTGG-**C**-TGGATGGATG (SEQ ID NO 15)

including cytosine at the marked position, said sequence occurring at a position spanning approximately base pair 242 of the sequence of said gene having the sequence set forth as SEQ ID NO 26, and associating the presence of said adenine in said sequence with a predisposition to a higher rate of loss of bone mass than when cytosine is present.

Claim 27. (previously presented) A method as claimed in Claim 25 or 26, which further comprises determining the genotype of the promoter of the osteopontin gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the osteopontin gene, wherein said allelic variation is selected from (a) said promoter including the sequence

GTTTTTAGAATTTTC-**A**-GACTTCCCTCCACT (SEQ ID NO 21)

including adenine at the marked position rather than the sequence

GTTTTTAGAATTTTC-**G**-GACTTCCCTCCACT (SEQ ID NO 16)

including guanine at the marked position, said sequence occurring in the promoter at a position spanning approximately base pair 520 of the sequence of said gene having the sequence set forth as SEQ ID NO 27

and (b) said promoter including the sequence

GACAGAGGCAAGTT-**C**-TCTGAAGTCCTTGCA (SEQ ID NO 22)
including cytosine at the marked position rather than the sequence
GACAGAGGCAAGTT-**T**-TCTGAAGTCCTTGCA (SEQ ID NO 17)
including thymine at the marked position, said sequence occurring in the promoter at a position spanning approximately base pair 1825 of the sequence of said gene having the sequence set forth as SEQ ID NO 27, and associating said adenine in the sequence spanning base pair 520 with a predisposition to a higher rate of loss of bone mass than when guanine is present and the presence of said thymine in the sequence spanning base pair 1825 with a predisposition to a lower bone mass than when cytosine is present.

Claim 28. (previously presented) A method as claimed in Claim 25 or 26, which further comprises determining the genotype of the promoter of the osteoprotegerin gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the osteoprotegerin gene, wherein said allelic variation is said promoter including the sequence
GACCAGGGAATT-**G**-ATGGGGGAGACAGCGAA (SEQ ID NO 23)
including guanine at the marked position rather than the sequence
GACCAGGGAATT-**A**-ATGGGGGAGACAGCGAA (SEQ ID NO 24)
including adenine at the marked position, said sequence occurring in the promoter at a position spanning approximately base pair 163 of the sequence of said gene having the sequence set forth as SEQ ID NO 28, and associating the presence of said guanine in said sequence with a predisposition to a lower peak bone mass than when adenine is present.

Claim 29. (currently amended) A method as claimed in claim 25 or 26, comprising amplifying a relevant portion of the DNA of [a] <u>either or both of</u> said gene promoter<u>s</u> of said individual.

Claims 30. (currently amended) A method as claimed in Claim 29, wherein the sequence of said amplified portion or portions is determined by hybridization assay or by restriction fragment length analysis.

Claim 31 (previously presented) The method of claim 25, wherein the method comprises determining whether the individual is homozygous or heterozygous for both the allelic variation (a) and the allelic variation (b), and associating the combined presence of said adenine and said guanine with said predisposition to a lower peak bone mass.

Claim 32 (previously presented) A method as claimed in Claim 27, which further comprises determining the genotype of the promoter of the osteoprotegerin gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the osteoprotegerin gene, wherein said allelic variation is said promoter including the sequence
GACCAGGGAATT-**G**-ATGGGGGAGACAGCGAA (SEQ ID NO 23)
including guanine at the marked position rather than the sequence
GACCAGGGAATT-**A**-ATGGGGGAGACAGCGAA (SEQ ID NO 24)
including adenine at the marked position, said sequence occurring in the promoter at a position spanning approximately base pair 163 of the sequence of said gene having the sequence set forth as SEQ ID NO 28, and associating the presence of said guanine in said sequence with a predisposition to a lower peak bone mass than when adenine is present.

Claim 33. (currently amended) A method as claimed in claim 27, comprising amplifying a relevant portion of the DNA of [a] one or more of said gene promoters of said individual.

Claim 34. (currently amended) A method as claimed in claim 28, comprising amplifying a relevant portion of the DNA of [a] one or more of said gene promoters of said individual.

Claim 35 (previously presented) A method of assessing an individual's predisposition to a selected calcification condition status, namely a lower peak bone mass, which method comprises determining the genotype of the promoter of the bone sialoprotein gene (SEQ ID NO 25) to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the bone sialoprotein gene, wherein said allelic variation is selected from (a) said promoter including the sequence

ATATAGAAGCCCAAG-**G**-AAAATCAGCTGACC (SEQ ID NO 18)
including guanine at the marked position rather than the sequence
ATATAGAAGCCCAAG-**A**-AAAATCAGCTGACC (SEQ ID NO 13)
including adenine at the marked position, said sequence occurring in said promoter at a position spanning approximately base pair 1496 of the sequence of said gene having the sequence set forth as SEQ ID NO 25
and (b) said promoter including the sequence
ATAGTGAAAACTTGT-**A**-TAATTATGAAATTTT (SEQ ID NO 19)
including adenine at the marked position rather than the sequence
ATAGTGAAAACTTGT-**G**-TAATTATGAAATTTT (SEQ ID NO 14)
including guanine at the marked position, said sequence occurring in said promoter at a position spanning approximately base pair 1869 of the sequence of said gene having the sequence set forth as SEQ ID NO 25,
and associating the presence of said adenine in said sequence spanning base pair 1496 bp with a predisposition to a lower peak bone mass than when guanine is present and the presence of said guanine in said sequence spanning base pair 1869 bp with a predisposition to a lower peak bone mass than when adenine is present,
wherein the method further comprises the steps of:

(i) determining the genotype of the promoter of the matrix gla protein gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the matrix gla protein gene, wherein said allelic variation is said promoter including the sequence
TGGCTGGCTGGCTGG-**A**-TGGATGGATG (SEQ ID NO 20)

including adenine at the marked position rather than the sequence TGGCTGGCTGGCTGG-**C**-TGGATGGATG (SEQ ID NO 15) including cytosine at the marked position, said sequence occurring at a position spanning approximately base pair 242 of the sequence of said gene having the sequence set forth as SEQ ID NO 26, and associating the presence of said adenine in said sequence with a predisposition to a higher rate of loss of bone mass than when cytosine is present,

wherein the method further comprises the steps of:

(ii) determining the genotype of the promoter of the osteopontin gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the osteopontin gene, wherein said allelic variation is selected from (a) said promoter including the sequence GTTTTTAGAATTTTC-**A**-GACTTCCCTCCACT (SEQ ID NO 21) including adenine at the marked position rather than the sequence GTTTTTAGAATTTTC-**G**-GACTTCCCTCCACT (SEQ ID NO 16) including guanine at the marked position, said sequence occurring in the promoter at a position spanning approximately base pair 520 of the sequence of said gene having the sequence set forth as SEQ ID NO 27 and (b) said promoter including the sequence GACAGAGGCAAGTT-**C**-TCTGAAGTCCTTGCA (SEQ ID NO 22) including cytosine at the marked position rather than the sequence GACAGAGGCAAGTT-**T**-TCTGAAGTCCTTGCA (SEQ ID NO 17) including thymine at the marked position, said sequence occurring in the promoter at a position spanning approximately base pair 1825 of the sequence of said gene having the sequence set forth as SEQ ID NO 27, and associating said adenine in the sequence spanning base pair 520 with a predisposition to a higher rate of loss of bone mass than when guanine is present and the presence of said thymine in the sequence spanning base pair 1825 with a predisposition to a lower bone mass than when cytosine is

present; and

(iii) determining the genotype of the promoter of the osteoprotegerin gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the osteoprotegerin gene, wherein said allelic variation is said promoter including the sequence GACCAGGGAATT-**G**-ATGGGGGAGACAGCGAA (SEQ ID NO 23) including guanine at the marked position rather than the sequence GACCAGGGAATT-**A**-ATGGGGGAGACAGCGAA (SEQ ID NO 24) including adenine at the marked position, said sequence occurring in the promoter at a position spanning approximately base pair 163 of the sequence of said gene having the sequence set forth as SEQ ID NO 28, and associating the presence of said guanine in said sequence with a predisposition to a lower peak bone mass than when adenine is present.

Claim 36. (currently amended) A method as claimed in claim 35, comprising amplifying a relevant portion of the DNA of [a] <u>one or more of</u> said gene promoters of said individual.

Claim 37. (currently amended) A method as claimed in Claim 36, wherein the sequence of said amplified portion <u>or portions</u> is determined by hybridisation assay or by restriction fragment length analysis.